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Genome-wide association with MRI atrophy measures as a quantitative trait locus for Alzheimer's disease

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Abstract

Alzheimer's disease (AD) is a progressive neurodegenerative disorder with considerable evidence suggesting an initiation of disease in the entorhinal cortex and hippocampus and spreading thereafter to the rest of the brain. In this study, we combine genetics and imaging data obtained from the Alzheimer's Disease Neuroimaging Initiative and the AddNeuroMed study. To identify genetic susceptibility loci for AD, we conducted a genome-wide study of atrophy in regions associated with neurodegeneration in this condition. We identified one single-nucleotide polymorphism (SNP) with a disease-specific effect associated with entorhinal cortical volume in an intron of the *ZNF292* gene (rs1925690; P-value = 2.6×10^{-8} ; corrected P-value for equivalent

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number of independent quantitative traits = 7.7×10^{-8}) and an intergenic SNP, flanking the *ARPP-21* gene, with an overall effect on entorhinal cortical thickness (rs11129640; P-value = 5.6×10^{-8} ; corrected P-value = 1.7×10^{-7}). Gene-wide scoring also highlighted *PICALM* as the most significant gene associated with entorhinal cortical thickness (P-value = 6.7×10^{-6}).

Keywords

Alzheimer's disease; imaging-genetics; quantitative trait

Introduction

The US NIH Alzheimer's Disease Neuroimaging Initiative (ADNI)¹ and the European Union FP6-funded AddNeuroMed study² have complementary goals. ADNI is a 5-year public–private partnership investigating the effectiveness of integrating neuroimaging, genetic/biological markers, as well as clinical and neuropsychological assessments in measuring the progression of mild cognitive impairment (MCI) and early Alzheimer's disease (AD). The main aim of the AddNeuroMed study, also a private–public partnership and a pilot for the European FP6 Innovative Medicines Initiative, is to find biomarkers for AD, in particular for early diagnosis of the disease. Both projects have acquired similar data, and in this study, we integrate neuroimaging and genetic data obtained from the two projects to identify novel susceptibility loci for AD.

Research to identify genetic factors that predispose to AD recently resulted in the publication of two large-scale genome-wide association studies (GWASs). Harold et al.³ analyzed >16000 individuals in a two-stage case–control analysis, identifying, in addition to *APOE*, two loci that were significantly associated with AD (namely *CLU* and *PICALM*). Another large-scale study by Lambert et al.⁴ also found association with the *CLU* locus and additionally with the *CRI* locus. These findings have elucidated some of the genes that are causally implicated in predisposition to AD. However, the diseased case versus normal control design of these GWASs and the studies that preceded them have an inherent confound in that a proportion of the apparently normal control population will already harbor disease because of the long clinically silent prodromal phase. One way to address this confound is the use of endophenotypes of disease—that is, markers of pathology *in vivo* that can be used to separate diseased from normal individuals more accurately than can be achieved by clinical assessment alone, and hence have the potential for greater power than studies using the standard AD/normal case–control design. One approach to endophenotypes as a marker of disease in genetic studies is the use of imaging measures in a quantitative trait (QT) analysis.

This imaging-genetics approach has been undertaken by a number of previous studies in AD. Potkin et al.⁵ identified a number of loci potentially associated with hippocampal atrophy in a subset of the ADNI cohort (AD and control samples). Shen et al.⁶ combined whole-genome genotyping data with 142 measures of gray matter density, volume and cortical thickness in the full ADNI cohort. However, they focused on the main effects of each single-nucleotide polymorphism (SNP) and did not investigate disease-specific effects.

In this study, we integrate magnetic resonance imaging (MRI) measures and genome-wide common variation data in a combined data set of 939 subjects (236 AD, 424 MCI and 279 controls) from the AddNeuroMed² study and the ADNI;¹ both these public-private partnerships having common objectives and, critically for this analysis, common genetics and imaging protocols.^{7,8} We had two aims: (1) to carry out a GWAS of AD-related brain regions and (2) to investigate the influence of AD-related genes and loci reported by recent large-scale GWASs for AD,^{3,4} specifically, the *CLU*, *PICALM* and *CR1* loci. We focus on brain regions that are unequivocally affected by AD-related neurodegeneration, namely the hippocampus and entorhinal cortex, and also on the related measures whole-brain volume (WBV) and total ventricular volume (VV). We use these MRI-derived measures as QTs to determine disease-specific common variants associated with neural atrophy in patients with AD.

Materials and methods

Samples

A total of 281 subjects were selected from the AddNeuroMed study, a prospective, longitudinal multicenter study, to discover biomarkers for AD.² Data were collected from six medical centers across Europe: University of Kuopio (Finland), University of Perugia (Italy), Aristotle University of Thessaloniki (Greece), King's College London (United Kingdom), Medical University of Lodz (Poland) and University of Toulouse (France). Informed consent was obtained for all subjects, and protocols and procedures were approved by the relevant institutional review board at each data acquisition site. Neuropsychological tests were conducted at baseline. None of the MCI and AD subjects had other neurological or psychiatric disease, significant unstable systemic illness or organ failure and alcohol or substance misuse. AD diagnosis was made using the NINCDS-ADRDA (National Institute of Neurological and Communicative Disease and Stroke and Alzheimer's disease) criteria for probable AD.⁹ At baseline, all MCI subjects fulfilled the diagnostic criteria for amnesic MCI.^{10,11} A total of 281 patients were genotyped (94 AD, 96 MCI and 91 controls) and underwent MRI.

Data for 818 ADNI subjects were downloaded from the ADNI database (<http://www.loni.ucla.edu/ADNI>), including baseline 1.5-T MRI scans, Illumina genotyping data (Illumina, San Diego, CA, USA), demographic and neuropsychological information, *APOE* genotype and baseline diagnosis information (see Supplementary Methods for details).

Genotyping

Genotyping for all samples was performed using the Illumina HumanHap610-Quad BeadChips, which contain 620 901 markers. ADNI genotyping was conducted as described previously.⁶ AddNeuroMed genotyping was performed by the CNG (Centre National de Génotypage CNG, France) (see Supplementary Methods for details). The *APOE* genotype was obtained separately using standard methods.

AddNeuroMed and ADNI genotyping data were merged, and any ambiguous or uncalled SNPs were removed using PLINK.¹² SNPs with call rates < 98% or minor allele frequencies

<5% were excluded. The Hardy–Weinberg equilibrium was assessed in control samples and SNPs with Hardy–Weinberg equilibrium $<10^{-5}$ were excluded. A total of 488 911 SNPs passed quality control protocols. Individual samples with SNP call rates <98% were excluded. Gender and relatedness tests were conducted in PLINK. Individuals with incongruous or ambiguous SNP genders compared with clinical genders were excluded. In cases in which pairs of samples were related ($PI-HAT > 0.1875$), one of the samples was removed at random. Ethnicity information was available for all participants. To restrict the analysis data set to Caucasian samples, so as to avoid confounding effects due to differing allele frequencies in other populations, the samples were merged with the Hapmap phase 3 populations,¹³ and a population stratification analysis was conducted using Eigenstrat.¹⁴ Samples classified as non-European were excluded based on ethnicity information and Eigenstrat analysis (AddNeuroMed $n=0$, ADNI $n=64$). Overall, 1004 samples passed these quality control filters (AddNeuroMed $n=278$, ADNI $n=726$). The genotyping rate in these samples was 0.998.

Imaging

Data acquisition—Data acquisition for AddNeuroMed¹⁵ and ADNI⁸ took place using 1.5-T MR systems using a common protocol, which included a high-resolution sagittal three-dimensional T1-weighted MPRAGE volume (voxel size $1.1 \times 1.1 \times 1.2 \text{ mm}^3$) and axial proton density/T2-weighted fast spin echo images. Full brain and skull coverage was required for both of the latter data sets, and a detailed quality control was carried out on all MR images using the AddNeuroMed QC framework.¹⁵ All MR images received a clinical read by a radiologist to exclude any subjects with non-AD-related pathologies.

AddNeuroMed and ADNI image analysis—A highly automated structural MRI image processing pipeline developed by Fischl and Dale¹⁶ and Fischl *et al.*^{17,18} and producing both regional cortical thickness measures and regional volume measures was used for data analysis. Cortical reconstruction and volumetric segmentation included removal of the nonbrain tissue using a hybrid watershed/surface deformation procedure, automated Talairach transformation, segmentation of the subcortical white matter and deep gray matter volumetric structures (including the hippocampus, amygdala, caudate, putamen, ventricles) intensity normalization, tessellation of the gray matter–white matter boundary, automated topology correction and surface deformation following intensity gradients to optimally place the gray/white and gray/cerebrospinal fluid borders at the location where the greatest shift in intensity defines the transition to the other tissue class. Surface inflation was followed by registration to a spherical atlas, which used individual cortical folding patterns to match cortical geometry across subjects and parcellation of the cerebral cortex into units based on gyral and sulcal structures. All volumes were normalized by the subject's intracranial volume (ICV).

Regional cortical thickness was measured from 34 areas, and regional cortical volume was measured bilaterally from 24 areas. In total, images obtained from 1097 AddNeuroMed and ADNI samples passed imaging quality control and produced normalized WBVs. Measures for total hippocampal volume (HPV), VV, total entorhinal cortical volume (ERV) and mean (of left and right) entorhinal cortical thickness were extracted for 1070 samples.

QT analysis

The four normalized (by ICV) volumetric measures WBV, HPV, VV, ERV and the cortical thickness measure mean (of left and right) entorhinal cortical thickness (ERT) were used as QTs in separate regression analyses. ERT was not normalized by ICV. Including ICV as a covariate in the ERT analysis produces very similar results (r of regression coefficients = 0.999), and ICV is not significant in any of the regressions. The numbers of samples that passed both imaging and genotyping quality control protocols and for which there were complete relevant phenotypic and demographic data were 963 (WBV) and 939 (HPV, VV, ERV and ERT).

QT analyses were implemented using the linear model function (--linear) in PLINK, which allows covariates to be included in the linear model.¹² Each QT was regressed on the number of minor alleles of the 478 081 autosomal SNPs passing quality control criteria, assuming an additive allele effect. A number of different linear models were analyzed:

1. The additive allele effect was ascertained in an initial model, including age, gender, *APOE* ϵ 4 allele dosage and disease status as covariates. Disease status was coded as a continuous variable in the model (controls=0, MCI=1, AD=2) to reflect the nonindependent nature of the three diagnosis states. The genomic inflation factor (based on median χ^2 of the additive term in the model) was calculated to investigate potential population stratification effects in the analysis. The genomic inflation factors for WBV, HPV and VV for this model were > 1.05, indicating potential population effects. The ERV and ERT analyses had genomic inflation factors of 1.01.
2. To allow for population effects, Eigenstrat¹⁴ was run using the 1004 samples that passed quality control. Seven significant eigenvectors were detected using Tracy–Widom statistics. Model 1 was re-run for WBV, HPV and VV, including the seven significant eigenvalues for each sample. The genomic inflation factors for WBV, HPV and VV for this model were 1.00, 1.00 and 1.01, respectively.
3. To detect SNP effects that may differ according to disease status, an interaction term for disease status and the additive allele effect was included in the third model. For ERV and ERT, the covariates age, gender, *APOE* ϵ 4 allele dosage and disease status were included in the model. For WBV, HPV and VV, significant eigenvalues were further added.

To allow for multiple testing of five QTs (namely WBV, HPV, VV, ERV and ERT) that are correlated (Supplementary Table 1), we applied Matrix Spectral Decomposition (see <http://gump.qimr.edu.au/general/daleN/matSpD/>), based on the study by Nyholt,¹⁹ to QTs, which results in an effective number of independent variables of 3, using VeffLi.

Gene analysis

We performed linkage disequilibrium (LD)-based SNP grouping in PLINK¹² on the results of our entorhinal cortical thickness analysis using the --clump command with default settings. We also performed a set-based analysis in PLINK, using SNPs ± 100 kb of *PICALM* and ± 750 kb of *ARPP-21* (because of the intergenic location of the significant

associated SNP) as sets of genes and permuting 10000 times. This analysis was implemented by PLINK as follows (from <http://pngu.mgh.harvard.edu/~purcell/plink/anal.shtml#set>): For the gene set, for each SNP, determine which other SNPs are in LD, above a certain threshold R (0.5). Perform standard single SNP QT analysis. For the set, select up to N 'independent' SNPs (as defined before) with P -values below $P(0.05)$. The best SNP is selected first; subsequent SNPs are selected in order of decreasing statistical significance, after removing SNPs in LD with previously selected SNPs. From these subsets of SNPs, the statistic for each set is calculated as the mean of these single SNP statistics. Permute the data set 10 000 times, keeping LD between SNPs constant (that is, permute trait). The empirical P -value for set (EMP1) is the number of times the permuted set statistic exceeds the original one for the set.

Finally, we used a novel method for calculating gene-based P -values from GWA results (see Supplementary Methods for details). We restricted our analysis to ~20 000 protein-coding genes annotated in Ensembl v56 and mapped them to SNPs if the SNP was within 20 kb of the annotated coordinates.

Imputation

To further investigate the evidence of association at the *PICALM*, *ARRP-21* and *ZNF292* loci, we imputed SNPs in the region ± 500 kb of *PICALM* and *ZNF292* and in ± 750 kb of the *ARRP-21* locus with minor allele frequency >0.01 and imputation quality scores >0.99 in the CEU Hapmap phase 2 population²⁰ and the 1000 Genomes project²¹ using Beagle²² and IMPUTE,²³ respectively, and applied the QT analysis.

Results

QT analysis

Previous work has shown brain atrophy in patients with AD to be most pronounced in hippocampal and entorhinal cortical regions, as well as in WBV in MRI studies.^{7,24–26} The decreases in these areas and the corresponding increase in ventricular volume in the participants in this study are congruent with previous findings (Supplementary Figure 1). Although there are significant correlations between the neuroimaging traits that we measured (Supplementary Table 1), we aimed to identify structure-specific variants associated with disease and markers of general neurodegeneration (Table 1).

In brief, 1118 subjects were genotyped using the Illumina 610K Beadchip, and standard sample and SNP quality control measures were implemented (see the 'Materials and methods' section). Samples classified as non-European were excluded based on ethnicity information and principal components analysis.¹⁴ Measures of entorhinal cortical thickness and volume, hippocampal volume, together with total brain and ventricular volumes were derived using automated regional analysis as described previously⁷ (see the 'Materials and methods' section). We implemented models with and without the SNP by disease interaction, the latter model allowing us to investigate the main SNP effect in addition to disease-associated SNP effects identified by the interaction term in the former model.

Quantile–quantile plots and Manhattan plots of the results are shown in Supplementary Figures 2–5.

This analysis identified one SNP (Table 2a) with a disease-specific effect associated with entorhinal cortical volume at the genome-wide significance threshold of $P < 5 \times 10^{-8}$ in an intron of the *ZNF292* gene (rs1925690; P -value = 2.6×10^{-8} ; corrected P -value for equivalent number of independent QTs = 7.7×10^{-8} ; Figure 1a) and an intergenic SNP, flanking the *ARPP-21* gene, with a main effect in entorhinal cortical thickness close to this threshold (rs11129640; P -value = 5.6×10^{-8} ; corrected P -value = 1.7×10^{-7} ; Figure 1b). Neither of these variants has been previously associated with neurodegeneration, nor is either significantly associated with AD in the recent GWASs.^{3,4} *ZNF292* encodes a putative zinc-finger protein of unknown function. The disease-specific effect of this SNP is shown in Supplementary Figure 6. The *ARPP-21* gene encodes a neuronal phosphoprotein enriched in regions of the brain receiving dopaminergic innervation.²⁷ In all, 29 SNPs representing 21 different loci have main effects with P -values $< 10^{-5}$ (Supplementary Table 2), and 24 SNPs representing 17 loci have disease-associated effects with P -values $< 10^{-5}$ (Supplementary Table 3). Imputation of variants proximal to the *ARPP-21* and *ZNF292* loci (see the ‘Materials and methods’ section) identified a number of additional variants at P -values $< 10^{-4}$ proximal to rs11129640 (Supplementary Figure 7), but none in the case of the *ZNF292* rs1925690 variant, Supplementary Figure 8). LD-based SNP grouping was carried out for the *ARPP-21* and *ZNF292* loci; however, this analysis did not reveal any further SNPs. A set-based analysis of the *ARPP-21* locus using SNPs ± 750 kb of *ARPP-21* as a set of genes and permuting 10 000 times, resulted in an empirical P -value $< 10^{-4}$ and revealed 5 SNPs at $P < 0.05$ passing the LD threshold (see the ‘Materials and methods’ section).

In light of recent large-scale GWASs for AD,^{3,4} we then sought to identify any corroboratory evidence in our analyses for the genome-wide significant variants at the *CLU*, *PICALM* and *CR1* loci from these studies. The rs11136000 SNP in clusterin identified by Harold *et al.*³ and Lambert *et al.*⁴ is not significantly associated with any of the imaging QTs, nor is the rs6701713 variant in *CR1* identified by Lambert *et al.*⁴ The *PICALM*-associated SNP rs3851179 identified by Harold *et al.*,³ the minor allele of which they found to have an odds ratio of 0.86, is associated with an increase in entorhinal cortical thickness (uncorrected $P < 0.05$; Table 2b) in our main effect analysis. We then performed LD-based SNP grouping in PLINK¹² on the results of our entorhinal cortical thickness analysis. This highlighted the intronic *PICALM* SNP rs642949 (uncorrected P -value = 9.6×10^{-5}) as being in LD with two further SNPs with P -values < 0.001 (Figure 2a). We also performed a set-based analysis in PLINK, using SNPs ± 100 kb of *PICALM* as a gene set and permuting 10 000 times. Of the 11 SNPs significant at $P < 0.05$, 5 variants were independently significant (based on an r^2 threshold of 0.5), resulting in an empirical P -value = 0.0034. To investigate the evidence of association at the *PICALM* locus further, we imputed SNPs with minor allele frequency > 0.01 and imputation quality scores > 0.99 in the CEU Hapmap phase 2 population²⁰ and the 1000 Genomes project²¹ using Beagle²² and IMPUTE,²³ respectively, and applied the QT analysis. Although none of the imputed SNPs reaches suggestive significance, there are a further eleven Hapmap phase 2 SNPs and five 1000 genome SNPs at P -values $< 10^{-3}$ (Figures 2b and c).

As there seemed to be multiple nominally positive SNPs in the region, we used a novel method for calculating gene-based P-values from GWA results (see the ‘Materials and methods’ section). We restricted our analysis to ~20 000 protein-coding genes annotated in Ensembl v56 and mapped them to genotyped SNPs within 20 kb of the annotated coordinates. We calculated gene-wide P-values using a modified Fisher's method to combine P-values from correlated tests and applied a local false discovery rate. This method identified *PICALM* as the most significant gene in the main entorhinal cortical thickness analysis (P -value = 6.7×10^{-6} ; false discovery rate = 0.039; Table 3). The *ARPP-21* gene was not significant in this analysis (false discovery rate = 1), most likely because of the most significant SNP being located outside our threshold of 20 kb. The method was also applied to the disease-specific entorhinal cortical volume analysis, revealing *ZNF292* as the thirty-fifth most significant gene (false discovery rate = 0.25).

Discussion

We present a genome-wide QT study for brain atrophy as an endophenotype for AD pathology of >900 participants from the ADNI and AddNeuroMed projects. To our knowledge, this is the largest study integrating imaging measures and genetics in AD. We selected brain regions known to be affected by AD (such as the hippocampus, entorhinal cortex and whole brain) and in which atrophy has been highlighted by previous MRI studies.^{7,24–26,28} MRI scans were processed to produce volumetric measures of these regions of interest and also entorhinal cortical thicknesses. Genotyping data (~478K SNPs) were integrated with the imaging traits in QT analyses.

We used this imaging QTL approach first for all subjects and then with disease status as an interaction effect because we reasoned that this study design would have greater power to detect disease susceptibility loci than a case versus control design. In the latter, more usual approach, the presence of clinically silent cases in the control group and susceptible but unaffected people presents a substantial confound. Using a measure of active disease as an endophenotype might help to overcome this problem.

Our design also includes a large number of MCI subjects, adding to the power of the study. However, many MCI subjects will not progress to AD and a recent meta-analysis by Mitchell *et al.*²⁹ showed an annual conversion rate of 8.1% and a cumulative proportion of 33.6% for MCI conversion to dementia, although it is noted that some studies show higher proportions of conversion, and in all studies, some MCI subjects fail to progress only because of death. Although the findings we report in this study will require replication, we note that despite the relatively small sample size compared with GWASs (1000 versus > 10 000) it is striking that we observe main SNP and disease-specific effects that reach nominal genome-wide significance (Table 2a).

The most significant SNP ($P = 6.54 \times 10^{-8}$; main ERT analysis) we identify is proximal to the *ARPP-21* gene, a regulator of calmodulin signaling, that is involved in the cellular cAMP signaling pathway, particularly in striatal medium spiny neurons.³⁰ Calmodulin signaling has been widely implicated in AD pathogenesis (see the study by O'Day and Myre³¹ for a review). In addition to identifying common variants that are associated with disease

susceptibility, we included an interaction term between disease status and the additive SNP effect in the analysis. Implementing this model with our QTs, we identified 24 SNPs correlated with the brain regions at P -values $<10^{-5}$ and one SNP $<10^{-6}$ (Supplementary Table 3). The most significant SNP (ERV; P -value = 3.45×10^{-8}) is in an intron in the *ZNF292* gene, which codes for a zinc-finger protein expressed in the brain.³² Our disease-specific analysis highlights the association between the minor allele of this SNP (rs1925690) and increased entorhinal cortical volume (Supplementary Figure 6) in AD subjects, whereas the converse is evident in control individuals.

Our analysis suggests further evidence for the *PICALM* locus in neurodegeneration. Using a genecentric approach, we identify a number of SNPs contributing to a locus association with entorhinal cortical thickness (Figure 2). The *PICALM* variant identified by Harold *et al.*³ and other more significant variants in our study are associated with less atrophy in the entorhinal cortex, suggesting a protective effect. The *PICALM* protein is involved in clathrin-mediated endocytosis, inhibition of which has recently been shown to decrease levels of amyloid- β in brain interstitial fluid in mice.³³

We have focused on a small number of regions known to be affected in AD and have conducted main and disease-specific effects for all SNPs in both the ADNI and the AddNeuroMed cohorts. Our study design was different from the previously published study of the ADNI cohort by Shen *et al.*⁶ in that we restricted our analysis to regions previously strongly implicated in the etiopathology of AD and reprocessed all neuroimages. This meant that we tested different phenotypes to those of Shen *et al.* in our combined ADNI and AddNeuroMed cohort. These differences and the design of the study by Shen *et al.* do not allow a direct comparison of the results, and we would consider that we have conducted an independent analysis of the data.

Our data provide further evidence of a causal role for *PICALM* in AD, demonstrate the power of endophenotype-genotype association studies and further identify two genes, namely *ARPP-21* and *ZNF292*, as putative risk factors for this devastating and common neurodegenerative disease.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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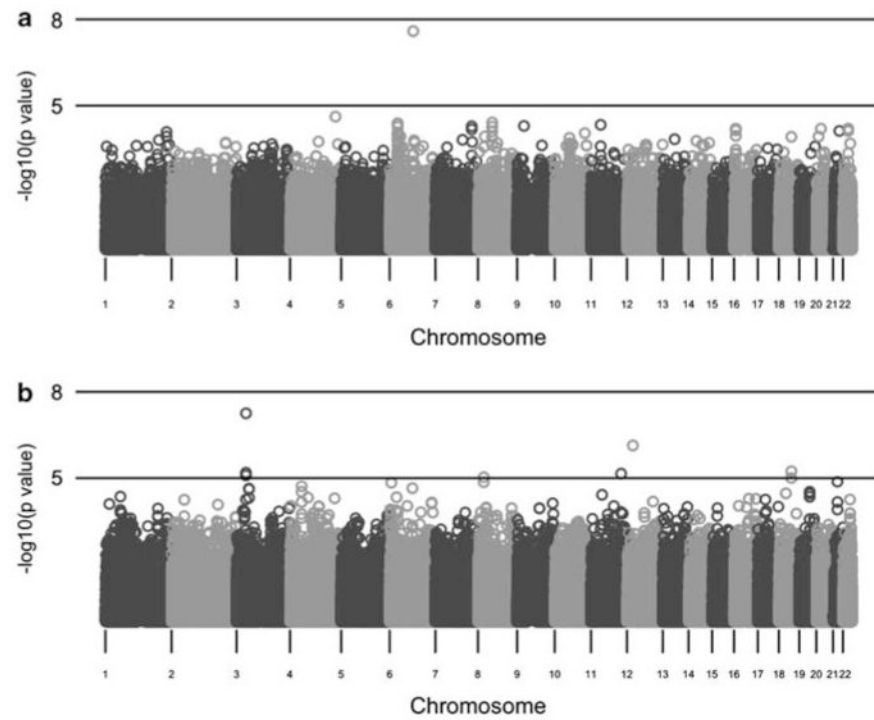


Figure 1.
(a) Manhattan plot of SNP effect P-values from the disease-specific entorhinal cortical volume analysis. (b) Manhattan plot of SNP effect P-values from the main entorhinal cortical thickness analysis. SNP, single-nucleotide polymorphism.

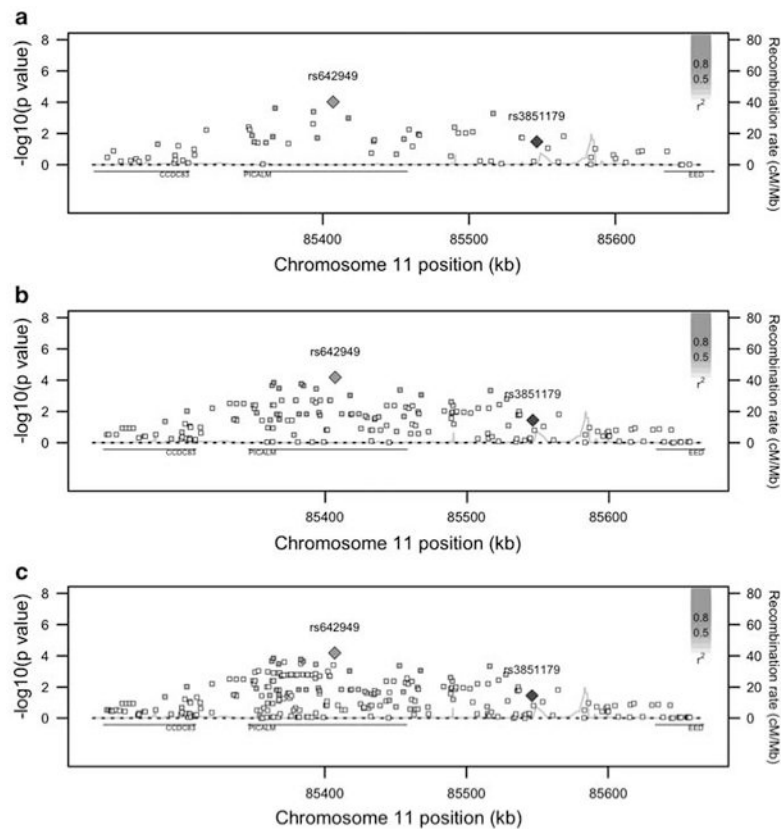


Figure 2.

SNP effect P -values from the main entorhinal cortical thickness analysis in the region surrounding PICALM for (a) original results (b) HapMap phase 2 SNPs and (c) 1000 Genomes Project SNPs. rs3851179 (in blue) is the SNP identified in the Harold et al.³ AD GWAS. Figure 2 was adapted from SNAP³⁴ output. AD, Alzheimer's disease; GWAS, genome-wide association study; SNP, single-nucleotide polymorphism. The color reproduction of this figure is available on the html full text version of the manuscript.

Table 1
Mean age, percentage female, mean *APOE* ε4 allele dosage and total *n* of control, MCI and AD subjects who passed the genetic and imaging quality control protocols for whole-brain volume (WBV) and all other (Other) quantitative trait analyses

	Control	MCI	AD
<i>WBV (N=963)</i>			
Age	74.99	74.86	75.38
Sex (% female)	49.3	39.2	51.8
<i>APOE</i> ε4	0.32	0.66	0.82
<i>n</i>	284	434	245
<i>Other (N=939)</i>			
Age	75.04	74.72	75.19
Sex (% female)	49.5	39.6	52.5
<i>APOE</i> ε4	0.30	0.66	0.83
<i>n</i>	279	424	236

Abbreviations: AD, Alzheimer's disease; MCI, mild cognitive impairment.

Table 2

(a) Uncorrected *P*-values for SNPs that have marginal genome-wide significance; (b) *PICALM* locus SNPs (*P*-value < 10⁻⁵) from Harold *et al.*³

(a)						
SNP	Chromosome	Position	Nearest gene	Relation to gene	Beta	Trait
rs11129640	3	35117515	ARPP-21	Intergenic	-0.124	ERT main
rs1925690	6	87923782	ZNF292	Intron	2.99 × 10 ⁻⁴	ERV disease
(b)						
SNP	Chromosome	Position	Nearest gene	Relation to gene	Beta	ERT <i>P</i> -value
rs3851179	11	85546288	PICALM	Intergenic	0.043	0.034
rs7941541	11	85536186	PICALM	Intergenic	0.049	0.019
rs543293	11	85497725	PICALM	Intergenic	0.054	0.009
rs1237999	11	85492678	PICALM	Intergenic	0.053	0.009
rs541458	11	85465999	PICALM	Intergenic	0.052	0.013
rs536841	11	85465472	PICALM	Intergenic	0.053	0.011
						1.9 × 10 ⁻⁸
						2.1 × 10 ⁻⁷
						6.9 × 10 ⁻⁷
						1.1 × 10 ⁻⁶
						2.3 × 10 ⁻⁶
						3.5 × 10 ⁻⁶

Abbreviations: AD, Alzheimer's disease; ERT, entorhinal cortical thickness; ERV, entorhinal cortical volume; GWAS, genome-wide association study; SNP, single-nucleotide polymorphism.
AD GWAS (GWAS *P*-value) and the uncorrected *P*-values in our main entorhinal cortex thickness (ERT *P*-value) quantitative trait analysis.

Table 3
Main entorhinal cortical thickness analysis gene-based results for genes with local FDR <0.1 (see the ‘Materials and methods’ section for details)

Ensembl ID	Gene symbol	P-value	FDR
ENSG00000073921	<i>PICALM</i>	6.66×10^{-6}	0.039
ENSG00000100266	<i>PACSIN2</i>	6.81×10^{-6}	0.039
ENSG00000175911	<i>ACI27496.2</i>	1.38×10^{-5}	0.050
ENSG00000196600	<i>SLC22A25</i>	2.10×10^{-5}	0.059
ENSG00000146067	<i>ACI45098.2</i>	2.16×10^{-5}	0.060
ENSG00000203724	<i>C1orf53</i>	2.97×10^{-5}	0.068
ENSG00000113811	<i>RPI1-884K10.1</i>	5.95×10^{-5}	0.088
ENSG00000124588	<i>NQO2</i>	6.01×10^{-5}	0.088
ENSG00000182747	<i>SLC35D3</i>	6.28×10^{-5}	0.090
ENSG00000176108	<i>CHMP6</i>	7.36×10^{-5}	0.095

Abbreviation: FDR, false discovery rate.